

(FILE 'HOME' ENTERED AT 13:18:28 ON 11 DEC 2007)

FILE 'REGISTRY' ENTERED AT 13:18:47 ON 11 DEC 2007

L1 9 S LSFAEPG/SQSP
L2 15032 S [LIMV] S [FWY] [AGPST] [ENDQ] [PAGST] [GAPST] /SQSP
L3 129 S L2 AND SQL<40
L4 4 S L2 AND SQL=13
L5 2 S L2 AND SQL=12
L6 4 S L2 AND SQL=11
L7 13 S L2 AND SQL=10
L8 10 S L2 AND SQL=9
L9 2 S L1 AND SQL=7

FILE 'HCAPLUS' ENTERED AT 13:21:56 ON 11 DEC 2007

L10 2 S L1 AND EPITOPE

=> s ;4
ENTER LOGIC EXPRESSION, QUERY NAME, OR (END):end
SEARCH ENDED BY USER

4 IS NOT A RECOGNIZED COMMAND

The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s l4 and epitope
4 L4
42073 EPITOPE
43843 EPITOPES
63788 EPITOPE
(EPITOPE OR EPITOPES)
L11 2 L4 AND EPITOPE

=> s l5 and epitope
2 L5
42073 EPITOPE
43843 EPITOPES
63788 EPITOPE
(EPITOPE OR EPITOPES)
L12 0 L5 AND EPITOPE

=> s l6 and epitope
4 L6
42073 EPITOPE
43843 EPITOPES
63788 EPITOPE
(EPITOPE OR EPITOPES)
L13 2 L6 AND EPITOPE

=> s l7 and epitope
15 L7
42073 EPITOPE
43843 EPITOPES
63788 EPITOPE
(EPITOPE OR EPITOPES)
L14 12 L7 AND EPITOPE

=> s l8 and epitope
14 L8
42073 EPITOPE
43843 EPITOPES
63788 EPITOPE

L15

(EPITOPE OR EPITOPES)
12 L8 AND EPITOPE

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165336_us-10-510-875a-2.dx.rag.

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GenCore version 6.2.1
(c) 1993 - 2007 Biocceleration,Ltd.

DM protein - protein search, using sw model

Run on: December 7, 2007, 23:02:13 ; Search time 904 Seconds

(without alignments)

3.996 Million cell updates/sec

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 3405708 seqs, 601679884 residues

total number of hits satisfying chosen Parameters:

3405708

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database : A_Geneseq_200711:*

1: geneseqP1980s:*

2: geneseqP1990s:*

3: geneseqP2000:*

4: geneseqP2001:*

5: geneseqP2002:*

6: geneseqP2003a:*

7: geneseqP2003b:*

8: geneseqP2004a:*

9: geneseqP2004b:*

10: geneseqP2005:*

11: geneseqP2006:*

12: geneseqP2007:*

RESULT 1

AAR48653 standard, peptide; 6 AA.

XAA AAR48653;

XX AAR48653;

AC AAR48653;

CC AAR48653;

DT 25-MAR-2003 (revised)

DT 21-SEP-1994 (first entry)

Result  Query

[tip://es/ScoreAccessWeb/GetItem.action?AppId=10510875&seqId=09323b67805b3adc&itemName=200...](http://es/ScoreAccessWeb/GetItem.action?AppId=10510875&seqId=09323b67805b3adc&itemName=200...) 12/11/200...

12/11/200...

SUMMARIES

ALIGNMENTS

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165338_us-10-510-875a-2.dx.rup.

Score.Home.Page Retrieve Application.List SCORE System.Overview SCORE FAQ Comments./ Suggestions

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US-10-510-875A-2

(without alignments)

77.206 Million cell updates/sec

Perfect score: 13

Sequence: 1 XXREXXS 6

Scoring table: BLOSUM62DX
Gapop 10.0 - Gapext: 0.5

Searched: 5032670 seqs, 1645091341 residues

total number of hits satisfying chosen parameters: 5032670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : UniProt_12.1:

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	13	100.0	8	1	UH09_RAT	P66575 rattus norvegicus
2	13	100.0	8	2	AON900_HUMAN	AON900 homo sapiens
3	13	100.0	8	2	Q80WDS_MUSPP	Q80WDS mus sprattus
4	13	100.0	8	2	Q9QVB8_DMUR	Q9QVB8 mus sp. mephisto
5	13	100.0	8	2	Q89K65_JC_POCVJC	Q89K65 jc polyomavirus
6	13	100.0	8	2	Q6PNU7_SV40	Q6PNU7 simian virus 40
7	13	100.0	8	2	Q6QSX9_SV40	Q6QSX9 simian virus 40
8	13	100.0	8	2	Q8PUD5_SV40	Q8PUD5 simian virus 40

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165338_us-10-510-875a-2.dx.rup.

Q6pujd9 simian virus

Q6PPE1_SV40

Q94vax varanus sal

Q94vb2 varanus sal

Q94vb5 varanus sal

Q94vb2 varanus yuw

Q7m3n7 gryllus bimaculatus

Q85v64 eucalyptus

Q91nb8 simian virus

Q9Pyk1 simian virus

Q94vi0 varanus giganteus

Q75gcs gallus lafayetensis

Q94vc6 varanus pilosissimus

Q15v8g gallus gallus

Q81626 locusta migratoria

Q7rz22 neurospora

Q7sa62_neuCR

Q5s4q0_homo sapiens

Q9twx1_dermatophagoides pteronyssinus

Q3yab8 macaca mulatta

Q85v67_eucalyptus

Q9Xmb4_aegilops tauschii

Q7SA62_NEUCR

Q5s4q0_HUMAN

Q9TPX1_DERCPA

Q28v77_eucalyptus

Q3XAH8_RACHMUS

Q85v67_EUCGR

Q9Xb4_AEGPTA

Q76v79_bk_polyomaviridae

Q53x11_bk_polyomaviridae

Q85bv6_EUCGR

Q53x32_bk_polyomaviridae

Q9QF11_mus_sp_pro

Q53x33_bk_polyomaviridae

Q76v79_bk_polyomaviridae

Q53x10_bk_polyomaviridae

Q53x12_POVKX

Q9X061_anolis_baeticus

Q94vg5_varanus_giganteus

Q94vd5_varanus_oli

P83067_bacillus_cephalinus

Q7s183_neurospora_crassa

Q29831_homo_sapiens

Q5fbx0_homo_sapiens

Q7M4J2_ASCSU

Q35374_PARTE

Q4YTF6_PLABE

Q7RMD3_PLAYVO

Rattus norvegicus (rat)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathia;

Muroidea; Muridae; Murinae; Rattus;

[1]

PROTEIN SEQUENCE,

STRAN_WISTAR; TISSUE=Heart;

RA Li X.-P., Pleissner K.-P., Scheeler C., Regitz-Zagrosek V., Salikov J., Jungblut P.R.;

http://es/ScoreAccessWeb/GetItem.action?AppId=10510875&seqId=0932367805b3ac7&itemName=200...

Q6pujd9 simian virus

Q6PPE1_SV40

Q94vax varanus sal

Q94vb2 varanus sal

Q94vb5 varanus sal

Q94vb2 varanus yuw

Q7m3n7 gryllus bimaculatus

Q85v64 eucalyptus

Q91nb8 simian virus

Q9Pyk1 simian virus

Q94vi0 varanus giganteus

Q75gcs gallus lafayetensis

Q94vc6 varanus pilosissimus

Q15v8g gallus gallus

Q81626 locusta migratoria

Q7rz22 neurospora

Q7sa62_neuCR

Q5s4q0_homo sapiens

Q9twx1_dermatophagoides pteronyssinus

Q3yab8 macaca mulatta

Q85v67_eucalyptus

Q9Xmb4_aegilops tauschii

Q7SA62_NEUCR

Q5s4q0_HUMAN

Q9TPX1_DERCPA

Q28v77_eucalyptus

Q3XAH8_RACHMUS

Q85v67_EUCGR

Q9Xb4_AEGPTA

Q76v79_bk_polyomaviridae

Q53x11_bk_polyomaviridae

Q85bv6_EUCGR

Q53x32_bk_polyomaviridae

Q9QF11_mus_sp_pro

Q53x33_bk_polyomaviridae

Q76v79_bk_polyomaviridae

Q53x10_bk_polyomaviridae

Q53x12_POVKX

Q9X061_anolis_baeticus

Q94vg5_varanus_giganteus

Q94vd5_varanus_oli

P83067_bacillus_cephalinus

Q7s183_neurospora_crassa

Q29831_homo_sapiens

Q5fbx0_homo_sapiens

Q7M4J2_ASCSU

Q35374_PARTE

Q4YTF6_PLABE

Q7RMD3_PLAYVO

Rattus norvegicus (rat)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathia;

Muroidea; Muridae; Murinae; Rattus;

[1]

PROTEIN SEQUENCE,

STRAN_WISTAR; TISSUE=Heart;

RA Li X.-P., Pleissner K.-P., Scheeler C., Regitz-Zagrosek V., Salikov J., Jungblut P.R.;

http://es/ScoreAccessWeb/GetItem.action?AppId=10510875&seqId=0932367805b3ac7&itemName=200...

Q6pujd9 simian virus

Q6PPE1_SV40

Q94vax varanus sal

Q94vb2 varanus sal

Q94vb5 varanus sal

Q94vb2 varanus yuw

Q7m3n7 gryllus bimaculatus

Q85v64 eucalyptus

Q91nb8 simian virus

Q9Pyk1 simian virus

Q94vi0 varanus giganteus

Q75gcs gallus lafayetensis

Q94vc6 varanus pilosissimus

Q15v8g gallus gallus

Q81626 locusta migratoria

Q7rz22 neurospora

Q7sa62_neuCR

Q5s4q0_homo sapiens

Q9twx1_dermatophagoides pteronyssinus

Q3yab8 macaca mulatta

Q85v67_eucalyptus

Q9Xmb4_aegilops tauschii

Q7SA62_NEUCR

Q5s4q0_HUMAN

Q9TPX1_DERCPA

Q28v77_eucalyptus

Q3XAH8_RACHMUS

Q85v67_EUCGR

Q9Xb4_AEGPTA

Q76v79_bk_polyomaviridae

Q53x11_bk_polyomaviridae

Q85bv6_EUCGR

Q53x32_bk_polyomaviridae

Q9QF11_mus_sp_pro

Q53x33_bk_polyomaviridae

Q76v79_bk_polyomaviridae

Q53x10_bk_polyomaviridae

Q53x12_POVKX

Q9X061_anolis_baeticus

Q94vg5_varanus_giganteus

Q94vd5_varanus_oli

P83067_bacillus_cephalinus

Q7s183_neurospora_crassa

Q29831_homo_sapiens

Q5fbx0_homo_sapiens

Q7M4J2_ASCSU

Q35374_PARTE

Q4YTF6_PLABE

Q7RMD3_PLAYVO

Rattus norvegicus (rat)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathia;

Muroidea; Muridae; Murinae; Rattus;

[1]

PROTEIN SEQUENCE,

STRAN_WISTAR; TISSUE=Heart;

RA Li X.-P., Pleissner K.-P., Scheeler C., Regitz-Zagrosek V., Salikov J., Jungblut P.R.;

http://es/ScoreAccessWeb/GetItem.action?AppId=10510875&seqId=0932367805b3ac7&itemName=200...

ALIGNMENTS

RESULT 1

QH09 RAT

ID UH09 RAT

Reviewed: P56575; 1998, integrated into UniProtKB/Swiss-Prot.

ON 15-DEC-1998, sequence version 1.

DT 24-JUL-2007, entry version 20.

DE Unknown protein from 2D-PAGE of heart tissue (spot P9) (fragment).

DS Rattus norvegicus (rat)

JC Eukaryota; Metazoa; Chordata; Craniata; Vertebrates; Euteleostomi;

JC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathia;

JC Muroidea; Muridae; Murinae; Rattus;

JN NCBI_TaxID=10116;

RN [1]

RP PROTEIN SEQUENCE,

RC STRAN_WISTAR; TISSUE=Heart;

RA Li X.-P., Pleissner K.-P., Scheeler C., Regitz-Zagrosek V., Salikov J., Jungblut P.R.;

http://es/ScoreAccessWeb/GetItem.action?AppId=10510875&seqId=0932367805b3ac7&itemName=200...

12/11/2007

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SCORE Results Details for Application 10510875 and Search Result 20071207_165415_us-10-510-875a-6.rag.

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CM protein - protein search, using sw model

Perfect score: 36

Sequence: 1 LSPAEFG 7

Scoring table: BLOSUM62

Gapop 11.0 , Gapext 0.5

3405708 seqs, 60187984 residues

total number of hits satisfying chosen parameters: 3405708

minimum DB seq length: 0

maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 10*

Listing first 50 summaries

Database : A_Geneseq_200711:*

1: geneseqP1980s:*

2: geneseqP1990s:*

3: geneseqP2000:*

4: geneseqP2001:*

5: geneseqP2002:*

6: geneseqP2003a:*

7: geneseqP2003b:*

8: geneseqP2004a:*

9: geneseqP2004b:*

10: geneseqP2005:*

11: geneseqP2006:*

12: geneseqP2007:*

RESULT 1

ADE50785

ID ADE50785 standard; peptide; 7 AA.

XX

AC ADE50785;

XX

DT 29-JAN-2004 (first entry)

XX

Score 10510875

Length 7

DB ADE50785

Peptide ADE50785

Protein ADE50785

Human ADE50785

Score 10510875

Length 7

DB ADE50785

Peptide ADE50785

Protein ADE50785

Human ADE50785

Score 10510875

Length 7

DB ADE50785

Peptide ADE50785

Protein ADE50785

Human ADE50785

Score 10510875

Length 7

DB ADE50785

Peptide ADE50785

Protein ADE50785

Human ADE50785

No.	Score	Match	Length	DB	ID	Description
1	36	100.0	7	7	ADE50785	Protein k
2	36	100.0	10	7	ADE50782	Protein k
3	36	100.0	10	7	ADE50786	Protein k
4	36	100.0	10	7	ADE50781	Protein k
5	36	100.0	10	7	ADE50789	Protein k
6	36	100.0	10	12	AEN53756	Kinase no
7	36	100.0	10	12	AFB67165	Substrate
8	36	100.0	11	7	ADE50790	Protein k
9	36	100.0	11	7	ADE50787	Protein k
10	36	100.0	11	7	ADE50788	Protein k
11	36	100.0	11	12	AHS55968	Serine/Thr
12	36	100.0	11	12	AHS55989	Serine/Thr
13	36	100.0	13	7	ADE50791	Protein k
14	36	100.0	13	12	AFB67160	Substrate
15	33	91.7	189	10	AEB3363710	L. pneumo
16	33	91.7	189	10	AEB339786	L. pneumo
17	33	91.7	484	4	AAB76522	Corynebac
18	33	91.7	491	4	AAB65789	C. Glutam
19	33	91.7	491	4	AAG90675	C. glutami
20	33	91.7	491	6	ADL55551	C. Glutam
21	32	88.9	8	5	AAE23344	Human GSK
22	32	88.9	11	5	AAE23345	Human GSK
23	32	88.9	11	11	AEE22422	Fluoresce
24	32	88.9	11	11	AEG22422	Akt1 assa
25	32	88.9	13	6	ABP50423	Akt speci
26	32	88.9	13	6	ABP54026	Akt speci
27	32	88.9	13	6	AAE29760	Akt speci
28	32	88.9	13	6	AAG7962	Human Akt
29	32	88.9	13	6	ABB93474	Amino aci
30	32	88.9	13	7	AAO04278	Akt pepti
31	32	88.9	13	7	ADD96165	Biotin 1a
32	88.9	13	7	13	ADU48697	Akt pepti
33	32	88.9	13	7	ADU48653	Akt pepti
34	32	88.9	13	7	ADE15867	Peptide s
35	32	88.9	13	8	ADK2126	Akt pepti
36	32	88.9	13	8	ADO33600	Biotinyl
37	32	88.9	13	8	ADU48697	Akt pepti
38	32	88.9	13	8	ADU48583	Akt pepti
39	32	88.9	13	8	ADU48747	Akt pepti
40	32	88.9	13	8	ADU48568	Akt pepti
41	32	88.9	13	10	AED0288	Akt pepti
42	32	88.9	13	11	AEP27504	Akt pepti
43	32	88.9	13	11	AEE19201	Akt subst
44	32	88.9	13	11	AE144991	GSK3alpha
45	32	88.9	13	11	AE167776	Human Akt
46	32	88.9	13	11	Aej15815	Checkpoint
47	32	88.9	13	11	Aej15056	Rhuman CTRK
48	32	88.9	13	11	Aej15085	Peptide s
49	32	88.9	13	11	AEK42820	Akt pepti
50	32	88.9	13	12	AEL43685	Human Akt

ALIGNMENTS

Result	Query	Summaries	URL
12:	geneseqP2007:*	RESUME	http://es/ScoreAccessWeb/GetItem.action?AppId=10510875&seqId=09323b67805b3ad0&itemName=200...

RA Venter J.C.;
 RL Submitted (PEB-2006) to the EMBL/GenBank/DBJ databases.
 DC :- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

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CC EMBL: AA00100002; ER22603_1; -; Genomic_DNA.
 DR InterPro: IPRO12938; GSDH.
 DR Pfam: PF0795; GSDH; 1.

PE Predicted;
 SQ SEQUENCE 372 AA; 40153 MW; 7522FCAa6A526171 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 372;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 LSFAEPG 7
 DB 110 LSFAEPG 116

RESULT 2
 29IE13_9HTV2 Unreviewed; 107 AA.

AC Q9IE13;
 DR 01-OCT-2000, integrated into UniProtKB/TREMBL.
 DR 01-OCT-2000, sequence version 1.

DR 24-JUL-2007, entry version 28.
 DS Envelope glycoprotein gp105 (Fragment).

DN Name=env;
 DS Human immunodeficiency virus 2.
 DC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 DC Lentivirus; Primate lentivirus group.
 RN NCBI_TaxId=11709;

RN [1]
 RP NUCLEOTIDE SEQUENCE
 RX MEDLINE=0414625; PubMed=10957727; DOI=10.1089/08892220050117069;
 RA Parreira R.; Esteves A.; Santos C.; Piedade J.; Venenno T.,
 RA Canas-Pereira W.F.;

RT "Genetic variability of human immunodeficiency virus type 2 C2V3
 region within and between individuals from Bissau, Guinea-Bissau, West
 Africa." ;
 RT AIDS Res. Hum. Retroviruses 16:1307-1312 (2000).

DR EMBL: AJ246915; CAB50502_1; -; Genomic_DNA.
 GO: GO:0019031; C:viral envelope; IPA:interPro.

DR InterPro: IPR000777; GP120.
 DR Gene3D: G3DSA:2.170.40.20; GP120; 1.
 DR Pfam: PF00516; GP120; 1.

PE A: Predicted;

RW Envelope protein.
 RX MEDLINE=0414625; PubMed=10957727; DOI=10.1089/08892220050117069;
 RA Parreira R.; Esteves A.; Santos C.; Piedade J.; Venenno T.,
 RA Canas-Pereira W.F.;

RT "Genetic variability of human immunodeficiency virus type 2 C2V3
 region within and between individuals from Bissau, Guinea-Bissau, West
 Africa." ;
 RT AIDS Res. Hum. Retroviruses 16:1307-1312 (2000).

DR EMBL: AJ246890; CAB5057_1; -; Genomic_DNA.
 GO: GO:0019031; C:viral envelope; IEA:InterPro.

DR InterPro: IPR000777; GP120.
 DR Gene3D: G3DSA:2.170.40.20; GP120; 1.
 DR Pfam: PF00516; GP120; 1.

PZ 4: Predicted;

RW Envelope protein.
 FT NON_TER 107 107 107 AA; 12578 MW; C06D9DA7EC3FCB32 CRC64;

SQ SEQUENCE 107 AA; 12550 MW; C6FBAP65EFB6BBS5 CRC64;

Query Match 94.4%; Score 34; DB 2; Length 107;

Best Local Similarity 85.7%; Pred. No. 47;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

<http://es/ScoreAccessWeb/GetItem.action?AppId=10510875&seqId=09323b67805b3ad7&itemName=200...> 12/11/200

RA Venter J.C.;
 RL Submitted (PEB-2006) to the EMBL/GenBank/DBJ databases.
 DC :- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

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CC EMBL: AA00100002; ER22603_1; -; Genomic_DNA.

DR InterPro: IPRO12938; GSDH.

DR Pfam: PF0795; GSDH; 1.

PE Predicted;
 SQ SEQUENCE 372 AA; 40153 MW; 7522FCAa6A526171 CRC64;

Query Match 100.0%; Score 36; DB 2; Length 372;
 Best Local Similarity 100.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 1 LSFAEPG 7
 DB 94 LSFAEPG 100

RESULT 3
 29IE18_9HTV2 Unreviewed; 107 AA.

AC Q9IDY8;
 DR 01-OCT-2000, integrated into UniProtKB/TREMBL.
 DR 01-OCT-2000, sequence version 1.

DR 24-JUL-2007, entry version 27.
 DS Envelope glycoprotein gp105 (Fragment).

DN Name=env;
 DS Human immunodeficiency virus 2.
 DC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 DC Lentivirus; Primate lentivirus group.

RN NCBI_TaxId=11709;

RN [1]
 RP NUCLEOTIDE SEQUENCE
 RX MEDLINE=0414625; PubMed=10957727; DOI=10.1089/08892220050117069;
 RA Parreira R.; Esteves A.; Santos C.; Piedade J.; Venenno T.,
 RA Canas-Pereira W.F.;

RT "Genetic variability of human immunodeficiency virus type 2 C2V3
 region within and between individuals from Bissau, Guinea-Bissau, West
 Africa." ;
 RT AIDS Res. Hum. Retroviruses 16:1307-1312 (2000).

DR EMBL: AJ246915; CAB50502_1; -; Genomic_DNA.
 GO: GO:0019031; C:viral envelope; IPA:interPro.

DR InterPro: IPR000777; GP120.
 DR Gene3D: G3DSA:2.170.40.20; GP120; 1.
 DR Pfam: PF00516; GP120; 1.

PZ 4: Predicted;

RW Envelope protein.
 FT NON_TER 107 107 107 AA; 12578 MW; C06D9DA7EC3FCB32 CRC64;

SQ SEQUENCE 107 AA; 12550 MW; C6FBAP65EFB6BBS5 CRC64;

Query Match 94.4%; Score 34; DB 2; Length 107;

Best Local Similarity 85.7%; Pred. No. 47;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

<http://es/ScoreAccessWeb/GetItem.action?AppId=10510875&seqId=09323b67805b3ad7&itemName=200...> 12/11/200

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This page gives you Search Results detail for the Application 10510875 and Search Result 20071207_165425_us-1

GenCore version 6.2.1
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JM protein - protein search, using sw model.

Run on: December 7, 2007, 23:12:02 ; Search time 39 Seconds
(without alignments)
17.270 Million cell updates/sec

Title:	US-10-510-875A-6
Perfect score:	36
Sequence:	1 LSPAPG 7
Scoring table:	BLOSUM62
	Gapop 10.0 , Gapext 0.5
Searched:	283416 seqs., 96216763 residues
total number of hits satisfying chosen parameters:	283416
minimum DB seq length:	0
maximum DB seq length:	2000000000
Post-processing:	Minimum Match 100% Maximum Match 100% Listing first 50 summaries
Database :	PIR_80_*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	% SUMMARIES				Description
	Score	Query Match	Length	DB ID	
1	33	91.7	223	2	hypothetical prote
2	32	88.9	124	2	protein kinase (EC
3	32	88.9	483	1	protein kinase (EC
4	31	86.1	623	2	ABC1 protein homolog
5	31	86.1	623	2	ABC1 protein homolog
6	31	86.1	2195	2	hypothetical prote
7	30	83.3	259	1	ovulation hormone
8	30	83.3	259	1	adenosylmethionine
9	30	83.3	373	2	probable carnitine
10	30	83.3	478	2	calcitonin receptor
11	30	83.3	478	2	carnitine receptor

Date: 0

ALIGNMENTS

Query Match http://es/ScoreAccessWeb/GetItem.action?AppId=1011010875&seqId=09323b67805b3ada&itemName=200... 12/11/200...

CORE Search Results Details for Application 10510875 and Search Result 20071207_165425_us-10-510... Page 3 of 2

CORE Search Results Details for Application 10510875 and Search Result 20071207_165425_us-10-510... Page 4 of 2

Best Local Similarity 85.7%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

2y 1 LSPAEPG 7
Db 198 LSPAEPG 204

RESULT 2

S1670 Protein kinase (EC 2.7.1.37) GSK-3-alpha - rabbit (fragments)
N;Alternate names: factor A; glycogen synthase kinase 3 alpha
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 08-Jun-1994 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: S1670
R;Woodgett, J. R.
EMBD J. 9., 2431-2438, 1990
A;Title: Molecular cloning and expression of glycogen synthase kinase-3/factor A.
A;Reference number: S14707; MUID:90316097; PMID:2164470
A;Molecule type: protein
A;Residues: 1-124 <WOO>
A;Cross-references: UNIPARC:UPI000017557A
C;Superfamily: Kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
P:39-92/Domain: protein kinase homology (fragments) <KIN>

Query Match 88.9%; Score 32; DB 2; Length 124;

Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

2y 2 SPAEPG 7
Db 3 SPAEPG 8

RESULT 4

T2007 ABC1 protein homolog T15B16.14 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004
R;Stonenberg, T.; Smith, R.
submitted to the EMBL Data Library, November 1998
A;Description: The sequence of A. thaliana T15B16.

A;Reference number: 214488
A;Accession: T2007
A;Status: translated from GB/EMBL/DBBJ
A;Molecule type: DNA
A;Residues: 1-623 <STO>
A;Cross-references: UNIPROT:Q9SB22; UNIPARC:UPI00000A3E05; EMBL:AF104919; NID:93859530; PID:93859605
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
A;Introns: 182/2; 257/3; 308/3; 361/3; 415/1; 490/3
A;Note: T15B16.14

Query Match 86.1%; Score 31; DB 2; Length 623;

Best Local Similarity 85.7%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
2y 1 LSPAEPG 7
Db 533 LSPAEPG 539

RESULT 5

T2128 ABC1 protein homolog [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
R;Dujardin, G.
submitted to the EMBL Data Library, December 1997
A;Reference number: 225969
A;Accession: T52128
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 1-623 <DU>
A;Cross-references: UNIPROT:065576; UNIPARC:UPI00000A25AB; EMBL:AJ001158; PID:CAP04557.1
A;Experimental source: ecotype Columbia; seedling
C;Genetics:
A;Note: ABC1AT

Query Match 86.1%; Score 31; DB 2; Length 623;

Best Local Similarity 85.7%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
2y 1 LSPAEPG 7
Db 533 LSPAEPG 539

RESULT 6

T34264 hypothetical protein F46c8.4 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T34264
R;Milcox, L.

<http://escoreaccessweb/getitem.action?appId=10510875&seqId=09323b67805b3ada&itemName=200...> 12/11/200...

<http://escoreaccessweb/getitem.action?appId=10510875&seqId=09323b67805b3ada&itemName=200...> 12/11/200...

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165336_us-10-510-875a-7.dx.rag.

Score, Home, Page Retrieve Application List SCORE System, Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 10510875 and Search Result 20071207_165336_us-10-510-875a-7.dx.rag.

[Go Back to previous page](#)[US-10-510-875A-7](#)[Perfect score: 33](#)[Sequence: 1 LXFPAEPG 7](#)

Scoring table: BLOSUM62DX Gapext 0 5

Searched: 3405708 seqs, 60187984 residues

Total number of hits satisfying chosen parameters: 3405708

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database :

A_Geneseq_200711:*

1: geneseqP1980s:*

2: geneseqP1990s:*

3: geneseqP2000:*

4: geneseqP2001:*

5: geneseqP002:*

6: geneseqP2003a:*

7: geneseqP2003b:*

8: geneseqP004a:*

9: geneseqP2004b:*

10: geneseqP2005:*

11: geneseqP2007:*

12: geneseqP2007:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query

No.	Score	Match Length	DB ID	Description
1	33	100.0	7 ADE50785	Ade50785 Protein k
2	33	100.0	10 ADE50782	Ade50782 Protein k
3	33	100.0	10 ADE50786	Ade50786 Protein k
4	33	100.0	10 ADE50781	Ade50781 Protein k
5	33	100.0	10 ADE50789	Ade50789 Protein k
6	33	100.0	10 AEN5756	Aen5756 Kinase no Afb67165 Substrate
7	33	100.0	10 AFB67165	Afb67165 Protein k
8	33	100.0	11 ADE50790	Ade50790 Protein k
9	33	100.0	11 ADE50787	Ade50787 Protein k
10	33	100.0	11 ADE50788	Ade50788 Protein k
11	33	100.0	11 AFE55968	Afe55968 Serine/Rhn Afh55989 Serine/Thr
12	33	100.0	11 AFH55989	Afh55989 Serine/Thr
13	33	100.0	13 ADE50791	Ade50791 Protein k
14	33	100.0	13 AFB67160	Afb67160 Substrate
15	33	100.0	98 AAU54359	AAU54359 Propionib
16	33	100.0	98 ABM50878	ABM50878 Propionib
17	33	100.0	296 Abm83500 M. xanthu	Abm83500 M. xanthu
18	33	100.0	345 AFZ46133 Recombina	AFZ46133 Recombina
19	33	100.0	420 ADX77623	ADX77623 Plant ful
20	33	100.0	426 ADY12256	ADY12256 Plant ful
21	33	100.0	426 ADY78935	ADY78935 Plant ful
22	33	100.0	484 AAB7522	AAB7522 Corynebac
23	33	100.0	491 AAB45789	Aab45789 C. glutam
24	33	100.0	491 AAG90675	AAG90675 C. glutam
25	33	100.0	491 ADL65551	ADL65551 C. glutam
26	33	100.0	832 ABO76120	ABO76120 Pseudomon
27	33	100.0	164 AEW22602	AEW22602 Tyzaccine
28	31	93.9	404 AEC55873	Aec55873 Goldfish
29	31	93.9	450 ABM22976	Abm22976 M. xanthu
30	31	93.9	1089 ADF191892	ADF191892 Agarase I
31	31	93.9	2195 ADN24175	ADN24175 Bacterial
32	30	90.9	53 ABP10072	ABP10072 Human ORF
33	30	90.9	53 ABP64040	ABP64040 Drosophil
34	30	90.9	68 ABB69113	ABB69113 Drosophil
35	30	90.9	68 AFCL4089	AFCL4089 Fruit fly
36	30	90.9	68 AFB98659	AFB98659 Fruit fly
37	30	90.9	146 ABT0246	ABT0246 Pseudomon
38	30	90.9	146 ADX96708	ADX96708 Plant ful
39	30	90.9	189 AEB35370	AEB35370 L. pneumo
40	30	90.9	189 AEB39786	Aeb39786 L. pneumo
41	30	90.9	197 ABO58613	ABO58613 Human gen
42	30	90.9	289 ARG90376	ARG90376 C. glutam
43	30	90.9	294 ADD1210	ADD1210 C. glutam
44	30	90.9	344 ADP85501	ADP85501 Aspergill
45	30	90.9	353 ABG12121	ABG12121 Novel hum
46	30	90.9	382 ABM86018	ABM86018 Rice abio
47	30	90.9	416 ADN21187	ADN21187 Bacterial
48	30	90.9	430 AES88756	Aes88756 S. agalac
49	30	90.9	430 AES93498	Aes93498 S. agalac
50	30	90.9	430 AES84218	Aes84218 S. agalac

ALIGNMENTS

RESULT 1
ADE50785 standard; peptide: 7 AA.
XX AC ADE50785;
XX DT 29-JAN-2004 (first entry)

http://es/ScoreAccessWeb/GetItem.action?AppId=10510875&seqId=09323b67805b3add&itemName=200... 12/11/200

Score_Home_Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions			
This page gives you Search Results detail for the Application 10510875 and Search Result 20071207_165341_us-1			
Copyright (c) 1993 - 2007 Biocceleration Ltd.			
DM Protein - Protein search, using sw model			
Run on: December 7, 2007, 23:05:54 ; Search time 19 Seconds (without alignments) 35.738 Million cell updates/sec			
Title: US-10-510-875A-7 Perfect score: 33 Sequence: 1 LXXAEPG 7			
Scoring table: BLOSUM62DX Gapop 10.0 , Gapext 0.5			
Searched: 283416 seqs, 96216763 residues			
Total number of hits satisfying chosen parameters: 283416			
Minimum DB seq length: 0 Maximum DB seq length: 2000000000			
Post-processing: Minimum Match 0% Maximum Match 100%			
Listing first 50 summaries			
Database : PIR:80:*			
1: pir1:*			
2: pir2:*			
3: pir3:*			
4: pir4:*			

Pred. No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	33	100.0	223	2	H75600	hypothetical protein
2	33	100.0	623	2	T02097	ABC1 protein homolog
3	33	100.0	623	2	TS2128	ABC1 protein homolog
4	31	93.9	2175	1	GRNTEBE	genomic polyprotein
5	31	93.9	2195	2	T34264	hypothetical protein
6	31	93.9	2214	1	A48548	genomic polyprotein
7	30	90.9	1319	2	S310850	hypothetical protein
8	30	90.9	256	2	T0097	hypothetical protein
9	30	90.9	373	2	B70819	probable carnitine
10	30	90.9	383	2	T39854	hypothetical protein
11	30	90.9	478	2	A17430	calcitonin receptor

<http://escoreaccessweb/getitem.action?ApplId=10510875&seqId=09323b67805b3ac6&itemName=200...>

<http://escoreaccessweb/getitem.action?ApplId=10510875&seqId=0323b67805b3ac6&itemName=200...>

RESULT 1

gr5600	hypothetical protein - Deinococcus radiodurans (strain R1)
C.Species: Deinococcus radiodurans	
C.Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004	
C.Accession: H75600	
R.White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; Haft, D.H.; Science 286, 1571-1577, 1999	
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.	
A.Reference number: A75250; MUID:20036396; PMID:10567266	
A>Status: preliminary	
A.Molecule type: DNA	
A.Residues: 1-223 <WHI>	
A.Cross-references: UNIPROT:Q9RZ84; UNIPARC:UPI000000C1610; GB:AE001862; NID:96460468; I	
A.Experimental source: strain R1	
C.Genetics:	
A.Gene: DRA0070	
A.Map position: 2	
Query Match	100.0%; Score 33; DB 2; Length 223;

ALIGNMENTS

SurfI family prote
hypothetical prote
probable cAMP-resp
glycoprotein B - b
ATP-dependent heli
probable membrane
protein kinase (EC
hypothetical prote
SurfI family prote
hypothetical prote
acetyl-CoA carboxy
seed albumin - mun
hypothetical prote
2,5-diketo-D-gluc
acetyl-CoA carboxy
acetyl-CoA carboxy
threonine synthase
probable lsr-fami
conserved hypothet
hypothetical prote
ferric enterobacti
threonine synthase
probable menE - My
hypothetical prote
metabolite transpo
UI snRNP 70K prote
hypothetical prote
conserved hypothet
1-aminoacylpropan
conserved hypothet
probable acetolact
acetolactate synth
hypothetical prote
hemocyanin chain a
hypothetical glyc

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165338_us-10-510-875a-7.dx.rup.

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Run on: December 7, 2007 23:04:20 ; Search time 149 Seconds

(without alignments)
77.206 Million cell updates/sec

Title: US-10-510-875A-7

Perfect score: 33

Sequence: 1 LXFAPG 7

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 5032670 seqS, 1645091341 residues

Total number of hits satisfying chosen Parameters:

5032670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 50 summaries

Database : UniProt 12.1:
1: uniprot_sprot:
2: uniprot_trembl:
* :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Description

Match Length DB ID

1 33 100.0 Q5LM62_SILPO

2 33 100.0 Q7W959_GREEL

3 33 100.0 Q4HJM3_9BACT

4 33 100.0 Q4HJM2_9BACT

5 33 100.0 Q4HJM1_9BACT

6 33 100.0 Q4HJM4_9BACT

7 33 100.0 Q4HJ01_9BACT

8 33 100.0 Q4HJM5_9BACT

Q5lm62 silicibacte

Q7W959 caenorhabdi

Q4hjm3 uncultured

Q4hjm6 uncultured

Q4hjm4 uncultured

Q4hj01 uncultured

Q4hjm5 uncultured

Q5LM62 SILPO

Q5LM62;

AC

Q5LM62;

ID

Q5LM62_SILPO

Unreviewed;

DT

01-FEB-2005,

integrated into UniProtKB/TREMBL.

DR

01-FEB-2005, sequence version 1.

DR

24-JUL-2007, entry version 10.

DE

Putative, uncharacterized protein.

DN

OrderedNames=SP03102;

Silicibacter pomeroyi.

DC

Bacteria; Proteobacteria; Alpha proteobacteria; Rhodobacterales;

DC

Rhodobactraceae; Silicibacter.

JX

NCBI_TAXID=89184;

[1]

RN

Nucleotide Sequence [LARGE SCALE GENOMIC DNA].

RC

STRAIN=ATCC-700808 / DSM 15171 / DS-3;

RX

PubMed=15602564; DOI=10.1038/nature03170;

RA

Moran M.A., Buchan A., Gonzalez J.M., Heidelberg J.F., Whitman W.B.,

CORE Search Results Details for Application 10510875 and Search Result 20071207_165338_us-10-510... Page 2 of 4

Q9hm7 uncultured
Q9hm6 uncultured
Azrj15 oryza sativ
Asggk3 prestocysti
Q9rz84 deinococcus

Q1wm27 dasypus nov
P9374 trichosurus un
Qsw9h9 meriones un
Asgy31 flavobacter
Q8s302 arabidopsis
ASInco flavobacter
Q0ldd4 herpetosiph

Q13iy3 burkholderi

A1if3 geobacillus
Qskvn9 geobacillus

Q5kv9 relsonia e

Q6tcs5 relsonia e

Q5p4g9 azosp

Q7f9d9 oryza sativ

Q650w6 oryza sativ

Q5lrf8 silicibacte

Q0kiz0 relsonia e

Q6etc5 relsonia e

Q2xtv0 oryza sativ

Q7x8g0 oryza sativ

Q65m06 oryza sativ

Q5lrb8 stilpo

Q2l20 ralhej

Q46tcs ralhej

Q3t8q0 oryza sativ

Q7x8g0 oryza sativ

Q65n06 oryza sativ

Akaero marine acti

A0u117 magnetospir

A3bj48 oryza sativ

Q46tcs ralhej

Q3t8q0 oryza sativ

Q1dbf2 myxococcus

Q2jf04 franria sp.

Q0jcy3 oryza sativ

Q2l20 ralhej

Q2evz4 xanthobacte

Q5m6v5 corynebacte

Q93kf1 corynebacte

A0r519 mycobacteri

A4gch2 corynebacte

A3turs oceanicola

Q55576 arthrobacter

Q9bb2 arabidopsis

Q0by76 hyphomonus

A0t012 cotesia plu

Q1gnq1 sphingopyxi

ALIGNMENTS

RESULT 1
25IM62_SILPO

Q5LM62;

0 AA.

Q5LM62_SILPO

Q5LM62;

0 AA.

CORE Search Results Details for Application 10510875 and Search Result 20071207_165338_us-10-510... Page 2 of 4

Q5lm62 silicibacte

Q7y959 caenorhabdi

Q4hjm3 uncultured

Q4hjm6 uncultured

Q4hjm4 uncultured

Q4hj01 uncultured

Q4hjm5 uncultured

Q4hjm2 silicibacter pomroyi.

Q5LM62 Proteobacteria; Alpha proteobacteria; Rhodobacterales;

Q5LM62_SILPO

Q5LM62;

0 AA.

Q5LM62_SILPO

Q5LM62;

SCORE Search Results Details for Application 10510875 and Search Result 20071207_165347_us-10-510-875a-2.dx.raii.

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GenCore version 6.2.1

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DOMAIN protein - protein search, using sw model

Run on: December 7, 2007, 23:06:38 : Search time 88 Seconds

(without alignments)

9.719 Million cell updates/sec

Title: US-10-510-875A-2

Perfect score: 13

Sequence: 1 XXXXXS 6

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 983262 seqs, 142787483 residues

Total number of hits satisfying chosen parameters:

983262

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 50 summaries

Issued_Patents_AA.*

1: /EMC_Celerra_SID52/prodata/1/iaa/5_COMB.pep:*

2: /EMC_Celerra_SID52/prodata/1/iaa/6_COMB.pep:*

3: /EMC_Celerra_SID52/prodata/1/iaa/7_COMB.pep:*

4: /EMC_Celerra_SID52/prodata/1/iaa/H_COMB.pep:*

5: /EMC_Celerra_SID52/prodata/1/iaa/PETUS_COMB.pep:*

6: /EMC_Celerra_SID52/prodata/1/iaa/RE_COMB.pep:*

7: /EMC_Celerra_SID52/prodata/1/iaa/backfillsi.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Match	Length	DB ID	Description
1	13 100.0	6 1	US-08-039-786-2	Sequence 2, Appli	
2	13 100.0	6 1	US-07-859-291C-19	Sequence 19, Appli	
3	13 100.0	6 1	US-07-781-590A-5	Sequence 5, Appli	

RESULT 1

US-08-039-786-2

: Sequence 2, Application US/08039786

: Patent No. 5556784

: GENERAL INFORMATION:

: APPLICANT: KAUVAR, LAWRENCE M.

: TITLE OF INVENTION: DETERMINATION OF CONCENTRATION BY

: TITLE OF INVENTION: AFFINITY TITRATION

: NUMBER OF SEQUENCES: 2

: CORRESPONDENCE ADDRESS:

: ADDRESS: MORRISON & FOERSTER

: STREET: 2000 Pennsylvania Ave. N.W., Suite 5500

: CITY: Washington, D.C.

<http://es/ScoreAccessWeb/GetItem.action?AppId=10510875&seqId=09323b67805b3aca&itemName=200...> 12/11/200...

12/11/200